

# Post-translational histone modifications panel (active motif)

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Updated date: May 6, 2021

 An abbreviated version of this protocol was published in eLIFE in Mar 2021

Age-related changes in polycomb gene regulation disrupt lineage fidelity in intestinal stem cells

DOI: 10.7554/eLife.62250

## Detailed protocol

Thank you for the question. The reason for doing the post-translational histone modifications panel was to quantify abundance of various histone marks in young and old midguts and to look for age-associated changes. We sent our samples (whole midguts flash frozen in liquid nitrogen, ~50 midguts per sample) to Active Motif (<https://www.activemotif.com/>), which is a company that performed the entire protocol and analysis. I've attached the protocol they performed on our samples specifically. Please contact the Active Motif for further support on the exact types of reagents, etc.

To answer your second question about alternatives to ChIP-seq, one could use CUT&RUN or CUT&TAG methods, which do not require as much input material.

Thank you!

## Related files

 Active Motif protocol.xlsx



**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Jasper, H. and Tauc, H. (2021). Post-translational histone modifications panel (active motif). Bio-protocol Preprint. [bio-protocol.org/prep1058](https://bio-protocol.org/prep1058).
2. Tauc, H. M., Rodriguez-Fernandez, I. A., Hackney, J. A., Pawlak, M., Ronnen Oron, T., Korzelius, J., Moussa, H. F., Chaudhuri, S., Modrusan, Z., Edgar, B. A. and Jasper, H. (2021). Age-related changes in polycomb gene regulation disrupt lineage fidelity in intestinal stem cells. eLIFE. DOI: [10.7554/eLife.62250](https://doi.org/10.7554/eLife.62250)

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